

Figure 1

Sequence Name:

GW.S.ctg16335-000003.31.0

Figure 1A

LLAPTGSFLRNCTQDGWSETFPRPNLACGVNVNDSSNEKRSYLLKLKVMYTVGYSSSLVM
LLVALGILCAFRLRHCTRNYIHMHLFVSFILRALSNFIKDAVLFSSDDVTYCDAHRGCKL
VMVLFXYCIMANYSWLLVEGSTFTHxLAISFFSERKYLQGFVAFGWGSPAIFVALWAIAR
HFLEDVGCWDINANASIWWIIRGPVILSILNFIILRILMRKLRTQETRGNEVSHYK
RLARSTLLIPLFGIHYIVFAFSPEDAMEIQLFF

Figure 1B

CTCTTGGCACCCACAGGTTCTTGTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCATAATCTGGCCTGTGGCGTTAATGTGAACGACTCTCCAACGAGAACGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCGTGTCCCTCATCCTCGTGCCCTGTCCAACTTCATCAAG
GACGCCGTGCTCTTCCTCAGATGATGTCACCTACTGCGATGCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTT

Figure 1C

TACTGCATCATGGCCAACACTACTCCTGGCTGCTGGTGGAAAGGCTTACCTCACACATNTC
CTCGCCATCTCCTTCTCTGAAAGAAAGTACCTCCAGGGATTGTGGCATTGGATGG
GGTTCTCCAGCCATTGGTGTGGCTATTGCCAGACACTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATATTCTGGTCCCTGTGATC
CTCTCCATCCTGATTAATTTCATCCTTTCATAAACATTCTAAGAATCCTGATGAGAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCATTATAAGGCCCTGCCAGGTCC
ACTCTCCTGCTGATCCCCCTTGGCATCCACTACATCGTCTCGCCTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTT

Figure 1D

CTCTTGGCACCCACAGGTTCTTGTCCGAAACTGCACACAGGATGGCTGGTCAGAAACC
TTCCCCAGGCATAATCTGGCCTGTGGCGTTAATGTGAACGACTCTCCAACGAGAACGG
CACTCCTACCTGCTGAAGCTGAAAGTCATGTACACCGTGGGCTACAGCTCCTCCCTGGTC
ATGCTCCTGGTCGCCCTTGGCATCCTCTGTGCTTCCGGAGGCTCCACTGCACTCGCAAC
TACATCCACATGCACCTGTTCGTGTCCCTCATCCTCGTGCCCTGTCCAACTTCATCAAG
GACGCCGTGCTCTTCCTCAGATGATGTCACCTACTGCGATGCCACAGGGCGGGCTGC
AAGCTGGTCATGGTGCTGTT
TACTGCATCATGGCCAACACTACTCCTGGCTGCTGGTGGAAAGGCTTACCTCACACATNTC
CTCGCCATCTCCTTCTCTGAAAGAAAGTACCTCCAGGGATTGTGGCATTGGATGG
GGTTCTCCAGCCATTGGTGTGGCTATTGCCAGACACTTCTGGAAGATGTT
GGGTGCTGGGACATCAATGCCAACGCATCCATCTGGTGGATATTCTGGTCCCTGTGATC
CTCTCCATCCTGATTAATTTCATCCTTTCATAAACATTCTAAGAATCCTGATGAGAAA
CTTAGAACCCAAGAAACAAGAGGAAATGAAGTCAGCATTATAAGGCCCTGCCAGGTCC
ACTCTCCTGCTGATCCCCCTTGGCATCCACTACATCGTCTCGCCTCTCCCCAGAG
GACGCTATGGAGATCCAGCTGTTTTT

Figure 2

Sequence Name:

GW.S.ctg16490-000000.17.0

Figure 2A

PTFILFSFQPGDKRTKHICVYWEGSEGGHWSTEGCSHVHSNGSYTKCKCFHLSSFAVLVA
LAPKDPVLTVITQVGLTISLLCLFLAILTFLLCRPIQNTSTSLLHLELSLCLFLAHLFLT
GINRTEPELCSIPIAGLLHFLYLAFCFTWMLLEGHLFLTVRNLKVANYTSTGRFKKRFMYP
VGYGIPAVIIAVSAIVGPQNYGTFTHCWLKLDKGFIWSFMGPVAVIILNLVVFYFQVLWIL
RSKLSSLNKEVSTIQLDTRVMTFKAISQLFILGCSWGLGFFMVEEVGKTIGSIIAYSFTII
NTLQGVLLFVVHCLLNQRQR

Figure 2B

CCCACTTTCATACTATTCTTTCCAGCCTGGTGACAAGAGAACAAAACATATCTGTGTC
TACTGGGAGGGATCAGAGGGAGGCCACTGGTCCACGGAGGGCTGCTCTCATGTGCACAGC
AACGGTTCTTACACCAAATGCAAGTGCTTCATCTGTCAGCTTGCCGTCCCTCGTGGCT
CTTGCCCCCAAGGAGGACCTGTGCTGACCGTGTACCCAGGTGGGCTGACCATCTCT
CTGCTGTGCCCTCTCCTGCCATCCACCTTCCCTGTGCCGCCATCCAGAACACC
AGCACCTCCCTCCATCTAGAGCTCTCCCTGCCCTCTCCTGGCCACCTCCCTGTTCTG
ACGGGCATCAACAGAACTGAGCCTGAGGTGCTGTGCTCCATATTGCAGGGCTGCTGCAC
TTCCTCTACCTGGCTTGCTTCACCTGGATGCTCCTGGAAGGGCTGCACCTCTCCTCACC
GTCAGGAACCTCAAGGTGGCCAACTAACCCAGCACGGCAGATTCAAGAACAGGTTCATG
TACCCCTGTAGGCTACGGGATCCCAGCTGTGATTATTGCTGTGTCAGCAATAGTTGGACCC
CAGAATTATGGAACATTACTCACTGTTGGCTCAAGCTTGATAAAGGATTATCTGGAGC
TTCATGGGCCAGTAGCAGTCATTATCTTGATAAACCTGGTGTCTACTTCCAAGTTCTG
TGGATTTGAGAACAAACTTCCCTCCCTCAATAAGAACAGTTCCACCATTCAGGACACC
AGAGTCATGACATTAAAGCCATTCTCAGCTATTATCCTGGGTGTTCTGGGCCTT
GGTTTTTATGGTTGAAGAACAGTAGGGAAAGACGATTGGATCAATATTGCATACTCATTC
ACCATCATCAACACCCTTCAGGGAGTGTGCTTTGTGGTACACTGTCTCCTTAATCGC
CAGGTAAGG

Figure 3

Sequence Name:

GW.S.ctg13100-000000.33.0

Figure 3A

QHSDAVHDLLLDVITWVGILLSLVCLLICIFTFCFFRGLQSDRNTIHKNLCISLFVAELL
FLIGINRTDQPACAVFAALLHFFFLAAFTWMFLEGVQLYIMLVEVFESEHSRRKYFYLVG
YGMMPALIVAVSAAVDYRSYGTDKVCWLRLDTYFIWSFIGPATLIIMNVIFLGIALYKMFH
HTAILKPESGCLDNIKLKINIPIKSIYIYIMYICMCV

Figure 3B

CAGCACAGTGATGCGGTCCATGACCTCCTCTGGATGTGATCACGTGGTTGGAATTTG
CTGTCCCTTGTGTTGTCCTGATTGCATCTCACATTGCTTTCCGGGGCTCCAG
AGTGACCGTAACACCATCCACAAGAACCTCTGCATCAGTCTTTGTAGCAGAGCTGCTC
TTCCTGATTGGGATCAACCGAACCTGACCAACCAATTGCCTGTGCTGTTTCGCTGCCCTG
TTACATTTCTTCTTCTGGCTGCCTCACCTGGATGTTCTGGAGGGGGTGCAGCTTAT
ATCATGCTGGTGGAGGTTTGAGAGTGAACATTACCGTAGGAAATACTTTATCTGGTC
GGCTATGGATGCCTGCACTCATGGCTGTGCAGCTGCAGTAGACTACAGGAGTTAT
GGAACAGATAAAAGTATGGCTCCGACTTGACACCTACTTCATTGGAGTTTATAGGA
CCAGCAACTTGATAATTATGCTTAATGTAATCTCCTGGATTGCTTATATAAAATG
TTTCATCATACTGCTAACTGAAACCTGAATCAGGCTGTCTGATAACATCAAGTTAAA
ATTAATATTCCAATTATAAAATCTATTATATGTATATGCATGTGTG

Figure 4

Sequence Name:

GW.A.ctg12444-000001.0.2

Figure 4A

GNVAVAFVYYKSIGPLLSSSDNFLLKPQNYDNSEEEERVISSVISVSMSSNPPTLYELEK
ITFTLSHRKTDYRSLCAFWNYPDTMNGWSSEGCELTYSNETHTSCRNCNLTHFAILM
SSGPSIIKDYNILTRITQLGIIISLICLAI CIFTFWFSEIQSTRTTIHKNLCCSLFLAE
LVFLVGINTNTNKFCIIAGLLHYFFLAFAWM CIEGIHLYLIVVGVIYNKGFLHKNFYI
FGYLSPAVVVGFSAAALGYRYYGTKVCWLSTENNFIWSFIGPACLIILVCIYKIVITI QK
SDDH

Figure 4B

GGCAATGTTGCAGTTGCATTGTATATTATAAGAGTATTGGTCCTTGCTTCATCATCT
GACAACCTCTTATTGAAACCTCAAATTATGATAATTCTGAAGAGGAGGAAAGAGTCATA
TCTTCAGTAATTCAGTCTCAATGAGCTCAAACCCACCCACATTATATGAACCTGAAAAA
ATAACATTTACATTAAGTCATCGAAAGGTACAGATAGGTATAGGAGTCTATGTGCATT
TGGAATTACTCACCTGATACCATGAATGGCAGCTGGTCTTCAGAGGGCTGTGAGCTGACA
TACTCAAATGAGACCCACACCTCATGCCGCTGTAAATCACCTGACACATTGCAATTG
ATGTCCTCTGGTCCTTCCATTGGTATTAAAGATTATAATATTCTACAAGGATCACTCAA
CTAGGAATAATTATTCACTGATTGTCTGCCATATGCATTTCACCTCTGGTCTTC
AGTGAATTCAAAGCACCAGGACAACAATTCACAAAAATCTTGCTGTAGCTTATTCTT
GCTGAACTGTTTCTTGTGGATCAATACAATAACTAATAAGCTCTGTCAATC
ATTGCCGGACTGCTACACTCTTTAGCTGCTTTGCATGGATGTGCATTGAAGGC
ATACATCTCATCTCATTGTTGGGTGTCACTACAACAAGGGATTTGCAACAAGAAT
TTTATATCTTGCTATCTAACGCCAGCCGTGGTAGTTGGATTTCGGCAGCACTAGGA
TACAGATATTATGGCACAACCAAAGTATGTGGCTAGCACCAGAAAACAACCTTATTGG
AGTTTATAGGACCAGCATGCCTAATCATTCTGTATGTATATAAAATTGTTATTACA
ATTCAAAAAGTGTGATGATCAT

Figure 5

Sequence Name:

GW.S.ctg12789-000004.100.0

Figure 5A

GAWATTGCSVAALYLDSTACFCNHSTSFAILQLYEVQGPEEESLLRTLSPVGCGVSFCA
LTTFLLFLVAGVPKSERTTVHKNLTFSLASAEGFLMTSEWAKANEACVAVTVAMHFLFL
VAFSWMLVEGLLWRKVVAVSMHPGPMRLYHATGWGPVPGIVAVTLAMLPHDYVAPGHC
WLNVHTNAIWAFVGPVLFVLTVS

Figure 5B

GGTGCCTGGGCCACACAGGCTGCTCCGTGGCTGCCCTGTACCTGGACTCCACCGCCTGC
TTCTGCAACCACAGCACAGCTTGCCATCTGCTGCAAATCTATGAAGTACAGAGAGGC
CCTGAGGAGGAGTCGCTGCTGAGGACTCTGTCATTTGTGGGCTGTGGCGTGTGCTTCTGC
GCCCTCACCAACCACCTCTTGCTCTCCTGGTGGCCGGGTCCCCAAGTCAGAGCGAAC
ACAGTCCACAAGAACCTCACCTCTCCCTGGCCTCTGCCGAGGGCTTCCTCATGACCAGC
GAGTGGGCCAAGGCCAATGAGGTGGCATGTGTGGCTGTCACAGTCGCAATGCACTTCCTC
TTTCTGGTGGCATTCTCCTGGATGCTGGTGGAGGGGCTGCTGCTGTGGAGGAAGGTGGTA
GCTGTGAGCATGCACCCGGGCCAGGCATGCGCTCTACCACGCCACAGGCTGGGGCGTG
CCTGTGGCATCGTGGCGTCACCTGGCATGCTCCCCATGACTACGTGGCCCCCGGA
CATTGCTGGCTCAATGTGCACACAAATGCCATCTGGCCTTCGTGGGCCTGTGCTCTTC
GTGCTGACTGTGAGC

Figure 6

Sequence Name:

GW.A.ctg12776-000000.33.0

Figure 6A

MKSPPRTTLCLMFIVIYSSKAALNWNYESTIHPILLHEHEPAGEEALRQKRAVATKSPTAE
EYTVNIEISFENASFLDPIKAYLNSLSFPIHGNNTDQITDILSINVTTVCRPAGNEIWCS
CETGYGWPWERCLHNLCQERDVFLPGHCHSCLKELPNGPFCLLQEDVTLNMRVRLNVG
FQEDLMNTSSALYRSYKTDLETARKGYGILPGFKGVTVTGFKSGSVVVTYEVKTPPSLE
LIHKANEQVQSLNQTYKMDYNSFQAVTINESNFFVTPEIIIFEGDTVSLVCEKEVLSSNV
SWRYEEQQLEIQNSSRFISIYTALFNNMTSVSKLTIHNIITPGDAGEYVCKLILDIFEYECK
KIDVMPIQILANEEMKVMCDNNPVSLNCCSQGNVNSKVEWKQEGKINIPIGTPETDIDS
SCSRYTLKADGTQCPSSGTTVIYTCEFISAYGARGSANIKVTFISVANLTITPDPISV
SEGQNFSIKCISDVSNYDEVWNTSAGIKIYQRFYTTTLDGAESVLTVKTSTREWNGT
YHCIFRYKNSYIATKDVIVHPLPLKLNIMVDPLEATVSCSGSHIHKCCIEEDGDYKVT
HTGSSSLPAAKEVNKKQVCYKHNFNASSVWCSKTVDCCHFTNAANNSVWSPSMKLNLV
PGENITCQDPVIGVGEPGKVIQKLCRFSNVPPSPESPIGGTITYKCVGSQWEEKRNDIS
APINSLLQMAKLIKSPSQDEMLPTYLKDLISIDKAEHIESSSPGSLGAIINILDLLSTV
PTQVNSEMMTIVLSTVNVLGKPVNTWKVLQQQWTNQSSQLLHSVERFSQALQSGDSPPL
SFSQTNVQMSMVIKSSHPETYQQRFVFPYFDLWGNVIDKSYLENLQSDSSIVTMAFP
LQAILAQDIQENNFAESLVMTTVSHNTMPFRISMFTKNNSPSGGETKCVFWNFRANN
TGGWDSSGCYVEEGDGDNVTCICDHLLTSFSILMSPDSPDPSLLGILLDIISYVGVGFSI
LSLAACLVVEAVVWKSVTKNRTSYMRHTCIVNIAASLLVANTWFIIVVAAIQDNRYILCKT
ACVAATFFIHFYLSVFFWMLTLGLMLFYRLVFILETSRSTQKAIAFCLGYGCPLAISV
ITLGATQPREVYTRKNVCWLNWEDTKALLAFAIPALIIVVVNITITIVVITKILRPSIGD
KPCQEKSSLFQISKSIGVLTPLGLTWGFLTTVFPGTNLVFHIIFAILNVQLFILLF
GCLWDLKQEALLNKFSLSRWSSQHSKTSLGSSPVFSMSSPISRRFNNLFGKTGTYNVST
PEATSSSLENSASSLLN

Figure 6B

ATGAAATCCCCAAGGAGAACCACTTGTGCCTCATGTTTATTGTGATTTATTCTTCAA
GCTGCACTGAACGGAAATTACGAGCTACTATTACATCCTTGAGTCTTCATGAACATGAA
CCAGCTGGTGAAGAGGCACTGAGGCCAAAACGAGCCGTTGCCACAAAAGTCCTACGGCT
GAAGAATAACACTGTTAATATTGAGATCAGTTGAAAATGCATCCTCCTGGATCCTATC
AAAGCCTACTTGAACAGCCTCAGTTCCAATTCATGGAATAACACTGACCAAATTACC
GACATTTGAGCATAAAATGTGACAACAGTCAGACCTGCTGGAAATGAAATCTGGTGC
TCCTGCGAGACAGGTTATGGTGGCCTCGGAAAGGTGCTTCACAATCTCATTGTCAA
GAGCGTGACGTCTCCCTCCCAGGGCACCATTCAGCTGGCTAAAGAAACTGCCTCCAA
GGACCTTTGCCTGCTTCAGGAAGATGTTACCCCTGAACATGAGAGTCAGACTAAATGTA
GGCTTCAAGAAGACCTCATGAACACTTCCTCCGCCCTATAGGTCTACAAGACCGAC
TTGGAAACAGCGTCCGGAAAGGGTACGGAATTTCACAGGCTCAAGGGGTGACTGTG
ACAGGGTTCAAGTCTGGAAGTGTGGTGTGACATATGAAGTCAGACTACACCACATCA
CTTGAGTTAACATAAAGCCAATGAACAAGTTGTCAGAGCCTCAATCAGACCTACAAA
ATGGACTACAACACTCCTTCAAGCAGTTACTATCAATGAAAGCAATTCTTGTACACCA
GAAATCATCTTGAAGGGGACACAGTCAGTCAGTGTGAAAGGAAGTTGTCTCC
AATGTGTCTGGCGCTATGAAGAACAGCAGTTGAAATCCAGAACAGCAGCAGATTCTCG
ATTACACCGCACTTCAACACATGACTCGGTGTCCAAGCTCACCACACACATC
ACTCCAGGTGATGCAGGTGAATATGTTGCAAACACTGATATTAGACATTTGAATATGAG
TGCAAGAAGAAAATAGATGTTATGCCCATCAAATTGGCAAATGAAGAAATGAAGGTG
ATGTGCGACAACAATCCTGTATCTTGAACGTGCTGCAGTCAGGGTAATGTTAATTGGAGC
AAAGTAGAATGGAAGCAGGAAGGAAAATAAATATTCCAGGAACCCCTGAGACAGACATA
GATTCTAGCTGCAGCAGATAACCCCTCAAGGCTGATGGAACCCAGTGCCCAAGCGGGTCG

TCTGGAACAACAGTCATCTACACTTGTGAGTTCATCAGTGCCTATGGAGCCAGAGGCAGT
GCAAACATAAAAGTGACATTCATCTCTGTGCCAATCTAACATAACCCCGACCCATT
TCTGTTCTGAGGGACAAAACCTTCTATAAAATGCATCAGTGTGAGTAACATATGAT
GAGGTTTATTGGAACACTCTGTGGAATTAAAATATACCAAGATTTATACCACGAGG
AGGTATCTTGATGGAGCAGAATCAGTACTGACAGTCAAGACCTGACCAGGGAGTGGAT
GGAACCTATCACTGCATATTAGATATAAGAATTACATACAGTATTGCAACCAAAGACGTC
ATTGTTCACCCGCTGCCCTCAAAGCTAACATCATGGTGTGATCCTTGGAAAGCTACTGTT
TCATGCAGTGGTCCCACATCAAGTGTGCAAGAGGAGATGGAGACTACAAAGTT
ACTTTCCATACGGGTCCTCATCCCTCCTGTCGAAAGAAGTTAACAAAAAACAGTG
TGCTACAAACACAATTCAATGCAAGCTCAGTTCTGGTGTCAAAAACGTTGATGTG
TGTTGTCACTTACCAATGCTGCTAATAATTCAAGTGTGAGGCCATCTATGAAGCTGAAT
CTGGTTCTGGGAAAACATCACATGCCAGGATCCCGTAATAGGTGTCGGAGAGGCCGGG
AAAGTCATCCAGAAGCTATGCCGGTCTCAAACGTTCCAGCAGCCCTGAGAGTCCCATT
GGCGGGACCATCACTTACAAATGTGAGGCTCCAGTGGCTAAGGCTTGATCAAGAGGCCCTCT
ATCTCTGCCCAATAAACAGTCTGCTCCAGATGGCTAAGGCTTGATCAAGAGGCCCTCT
CAGGATGAGATGCTCCCTACATACCTGAAGGATCTTCTATTAGCATAGACAAAGCGGAA
CATGAAATCAGCTCTCTGGGAGTCTGGGAGCCATTATTAACATCCTGATCTGCTC
TCAACAGTCCAACCCAAAGTAAATTCAAGAAATGATGACGCGACGTGCTCTACGGTTAAT
GTCATCCTGGCAAGCCCGTCTGAAACACCTGGAAGGTTTACAACAGCAATGGACCAAT
CAGAGTTCACAGCTACTACATTCAAGTGGAAAGATTCCCAAGCATTACAGTCGGGAGAT
AGCCCTCCTTGTCTCTCCAAACTAATGTGAGATGAGCAGATGGTAATCAAGTCC
AGCCACCCAGAAACCTATCAACAGAGGTTGTTCCCATACTTGACCTCTGGGCAAT
GTGGTCATTGACAAGAGCTATCTAGAAAACCTGAGTCGGATTGCTTGTACCATG
GCTTCCCAACTCTCCAAGCCATCCTGCCAGGATATCCAGGAAAATAACTTGCAGAG
AGCTTAGTGTGACAACCAACTGTCAGCCACAATACAACATGCCATTGAGGATTCAATG
ACTTTAAGAACAAATAGCCCTCAGGCGGCAAACGAAGTGTGCTCTGGAAACTCAGG
CTTGCCAACAAACACAGGGGGGTGGGACAGCAGTGGGTGCTATGTAGAAGAAGGTGATGGG
GACAATGTCACCTGTATCTGTGACCACCTAACATCATCTCCATCCTCATGCCCCGTGAC
TCCCCAGATCCTAGTTCTCTGGAAATACTCCTGGATATTATTTCTATGTTGGGGTG
GGCTTTCCATCTGAGCTTGGCAGCCTGCTAGTTGGAAGCTGTGGTGTGAAATCG
GTGACCAAGAACCGGACTTCTTATATGCGCCACACCTGCATAGTAATATGCTGCC
CTTCTGGTCGCCAACACCTGGTCATTGTGGTCGCTGCCATCCAGGACAATCGCTACATA
CTCTGCAAGACAGCCTGTGTCGGCTGCCACCTTCTCATCCACTTCTTACCTCAGCGTC
TTCTCTGGATGCTGACACTGGGCTCATGCTGTTCTATGCCCTGGTTTCATTCTGCAT
GAAACAAGCAGGTCCACTCAGAAAGCCATTGCCCTCTGCTGGCTATGGCTGCCACTT
GCCATCTCGGTACAGCCTGGGAGCCACCCAGCCCCGGAAAGTCTATACGAGGAAGAAT
GTCTGTTGGCTCAACTGGGAGGACACCAAGCCCTGCTGGCTTCGCCATCCCAGCACTG
ATCATTGTTGGTGGTGAACATAACCATCACTATTGTGGTACATCAGGAAAGTCTGAGGCT
TCCATTGGAGACAAGCCATGCAAGCAGGAGAAGAGCAGCCTGTTCAAGTCAAGAGC
ATTGGGGTCTCACACCACTCTGGGCTCACTTGGGTTTGGTCTCACCACGTGTT
CCAGGGACCAACCTTGTGTTCCATATCATATTGCCATCCTCAATGTCTCAGGGATTA
TTCATTTTACTCTTGGATGCCCTGGGACTGAAGGTACAGGAAGCTTGCTGAATAAG
TTTCATTGTCGAGATGGTCTTACAGCACTCAAAGTCAACATCCCTGGGTCATCCACA
CCTGTGTTCTATGAGTTCTCAATATCAAGGAGATTAACAATTGTTGGTAAAACA
GGAACGTATAATGTTCCACCCAGAAGCAACCAGCTCATCCCTGGAAAACATCCAGT
GCTTCTCGTTGCTCAAC

Figure 7

Sequence Name:

GW.S.ctg12776-000000.175.0

Figure 7A

ILNSKSISNWTIFDRRNSSYILLHSVNSFARRLFIDNIPVDISDVFIHTMGTISGDNIG
KNFTFSMRINDTSNEVTGRVLISRDELRKVPSQSQVISIAFPТИGAILEASLLENVTVNG
LVLSAILPKELKRISLIFEKISKSEERRTQCVGWHSVENRWDQQACKMIQENSQQAVCKC
RPSKLFTSFSILMSPHILESLILTYITYVGLGISICSLILCLSIEVLVWSQVTKTEITYL
RHVCIVNIAATLLMADWFIVASFLSGPITHHKGCVAATFFVHFFYLSVFFWMLAKALLI
LYGIMIVFHTLPKSVLVASLFSVGYGCPLAIAAITVAATEPGKGYLRPEICWLNWDMTKA
LLAFVIPALAIVVVNLTVTLVIVKTQRAAIGNSMFQEVRAlVRISKNIAILTPLGLTW
GFGVATVIDDRSLAFHIIFSLLNAFQFFILVFGTILDPKV

Figure 7B

ATTCTTAACAGCAAAAGCATCTCCAACGGACTTTCATTCTGACAGAAACAGCAGCTAT
ATCCTGCTACATTCACTCAGTCAACTCCTTGCAAGAAGGCATTCTAGATAACATCCCTGTT
GACATATCAGATGTCTTCAATTCTACTATGGGCACCCATATCTGGAGATAACATTGGA
AAAAATTCACTTTCTATGAGAATTAAATGACACCAGCAATGAAGTCAGTGGAGAGTG
TTGATCAGCAGAGATGAACCTCGGAAGGTGCCTCCCTCTCAGGTCACTCAGCATTGCA
TTTCCAACATTGGGCTATTTGGAAGCCAGTCTTGAAAATGTTACTGTAAATGGG
CTTGTCCCTGTGCCATTGCCCCAAGGAACCTAAAAGAATCTCACTGATTGAAAAG
ATCAGCAAGTCAGAGGAGAGGAGGACACAGTGTGTTGGCTGGCACTCTGTGAGAACAGA
TGGGACCAGCAGGCCTGAAAATGATTCAAGAAAACCTCCAGCAAGCTGTTGCAAATGT
AGGCCAAGCAAATTGTTACCTCTTCAATTCTTATGTCACCTCACATCTTAGAGAGT
CTGATTCTGACTTACATCACATATGTAGGCCTGGGCATTCTATTGCAAGCCTGATCCTT
TGCTTGTCCATTGAGGTCTAGTCTGGAGCCAAGTGACAAAGACAGAGATCACCTATT
GCCATGTGCATTGTTAACATTGCAAGCCACTTGTGATGGCAGATGTGGTTCAATT
GTGGCTTCTTCTTACTGGCCAATAACACACCACAAGGGATGTGTGGCAGCCACATT
TTGTTCAATTCTTACCTTCTGTATTCTGGATGCTGCAAGGCACCTCCTTATC
CTCTATGGAATCATGATTGTTCCATACCTTGCCAAAGTCAGTCTGGTGGCATCTCTG
TTTCAGTGGCTATGGATGCCATTGCTGCCATCACTGTTGCTGCCACTGAA
CCTGGCAAAGGCTATCTACGACCTGAGATCTGCTGGCTCAACTGGGACATGACCAAGCC
CTCCTGGCCTCGTGATCCCAGCTTGGCCATCGTGGTAGTAAACCTGATCACAGTCACA
CTGGTGATTGTCAAGACCCAGCGAGCTGCCATTGGCAATTCCATGTTCCAGGAAGTGAGA
GCCATTGTGAGAATCAGCAAGAACATGCCATCCTCACACCACCTCTGGACTGACCTGG
GGATTGGAGTAGCCACTGTCATCGATGACAGATCCCTGGCCTTCCACATTATCTTCTCC
CTGCTCAATGCATTCCAGGGTTCTCATCCTAGTGTGTTGGAACCACCTGGATCCAAAG
GTA

400266363 40024404

Figure 8

Sequence Name:

GW.S.ctg16790-000000.13.0

Figure 8A

GTGDWSSEGCSTEVRPEGTVCCCDHLTFALLLPTLDQSTVHILTRISQAGCCVSMIFL
AFTIILYAFRLRSRERFKSEDAPKIHVALGGSLFLLNLAFLVNNGSGSKGDAACWARGA
VFHYFLLCAFTWMGLEAFHLYLLAVRWFNTYFGHYFLKLSLVGWGLPALMVGITGSANSY
GLYTIRDRENRTSLELCWFRETTMYALYITVHGYFLITFLFGMVVLALVWKIFTLSRA
TAVKERGKNRKKVLTLLGLSSLVGVTWGLAIFTPLGLSTVYIFALFNSLQVDFYILIFY

Figure 8B

GGGACCACTGGAGACTGGTCTCTGAGGGCTGCTCCACGGAGGTCAAGACCTGAGGGGACC
GTGTGCTGCTGTGACCACCTGACCTTTTCGCCCTGCTCCTGAGACCCACCTGGACCAG
TCCACGGTGCAATATCCTCACACGCATCTCCAGGCAGGGCTGTGGGCTCTCCATGATCTC
CTGGCCTCACCAATTATTCTTATGCCTTCTGAGGCTTCCCAGGAGAGGTTCAAGTCA
GAAGATGCCCAAAGATCCACGTGGCCCTGGGTGGCAGCCTGTTCTCCTGAATCTGGCC
TTCTTGGTCAATGTGGGGAGTGGCTCAAAGGGGCTGATGCTGCTGCTGGGCCGGGG
GCTGTCTTCAACTACTCCTGCTCTGTGCCTCACCTGGATGGGCTTGAAAGCCTCCAC
CTCTACCTGCTCGCTGTCAAGGTCTTCAACACCTACTTCGGGACTACTTCCTGAAGCTG
AGCCTGGTGGCTGGGCCTGCCCTGATGGTCATCGGCACCTCTGGAGCTATGCTGGTTC
TACGGCCTTACACCATCCGTGATAGGGAGAACCGCACCTCTGGAGCTATGCTGGTTC
CGTGAAGGGACAACCATGTACGCCCTATATCACCGTCCACGGCTACTTCCTCATCACC
TTCCTCTTGGCATGGTGGCTGGCCCTGGTGGCTGGAAGATCTCACCTGTCCCGT
GCTACAGCGGTCAAGGGAGCGGGGGAGAACCGGAAGAAGGTGCTCACCTGCTGGCCTC
TCGAGCCTGGTGGGTGTGACATGGGGTTGCCATCTCACCCGTTGGCCTCTCCACC
GTCTACATCTTGCACCTTCAACTCCTGCAAGTTGATTTCATATTGATCTTCTAT

7 6 0 3 2 6 9 5 3 0 6 4 4 1

Figure 9

Sequence Name:

GW.S.ctg12776-000000.172.0

Figure 9A

NHILD TAA IS NWAF I P N K N A S S D L L Q S V N L F A R Q L H I H N N S E N I V N E L F I Q T K G F H I N H N
T S E K S L N F S M S M N N T T E D I L G M V Q I P R Q E L R K L W P N A S Q A I S I A F P T L G A I L R E A H L Q N V
S L P R Q V N G L V L S V V L P E R L Q E I I L T F E K I N K T R N A R A Q C V G W H S K R R W D E K A C Q M M L D I
R N E V K C R C N Y T S V V M S F S I L M S S K S M T D K V L D Y I T C I G L S V I L S L V L C L I I E A T V W S R V
V V T E I S Y M R H V C I V N I A V S L L T A N V W F I I G S H F N I K A Q D Y N M C V A V T F F S H F F Y L S L F F W
M L F K A L L I I Y G I L V I F R R M M K S R M M V I G F A I G Y G C P L I I A V T T V A I T E P E K G Y I R P E A C W
L N W D N T K A L X A F A I P A F V I V A V N L I V V L V V A V N T Q R P S I G S S K S Q D V V I I M R I S K N V A I L
T P L L G L T W G F G I A T L I E G T S L T F H I I F A L L N A F Q F I L L F G T I M D H K V

Figure 9B

A A C C A C A T C C T C G A C A C A G C A G G C A T T C A A A C T G G G C T T C A T T C C C A A C A A A A T G C C
A G C T C G G A T T T G T T G C A G T C A G T G A A T T G T T G C C A G A C A A C T C C A C A T C C A C A A T A A T
T C T G A G A A C A T T G T G A A T G A A C T C T C A T T C A G A C A A A A G G G T T C A C A T C A A C C A T A A T
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